

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 12:20:40 ; Search time 1692 Seconds
(without alignments)
764.885 Million cell updates/sec

Title: US-10-089-380-5

Perfect score: 34

Sequence: 1 gaagttcctatactttctggagaataggaaattc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32.4	95.3	74	9 CG654127	CG654127 OST420864
2	32.4	95.3	81	1 A1265023	A1265023 uk01f07.y
3	32.4	95.3	81	1 A1265111	A1265111 uk03c08.y
4	32.4	95.3	81	1 A1272501	A1272501 uk04g01.y
5	32.4	95.3	88	1 A1316311	A1316311 uj99a11.y
6	32.4	95.3	105	9 CG548652	CG548652 OST150646
7	32.4	95.3	112	9 CG606396	CG606396 OST284215
8	32.4	95.3	124	9 CG523627	CG523627 OST110354
9	32.4	95.3	130	9 CG526837	CG526837 OST110386
10	32.4	95.3	133	9 CG529602	CG529602 OST110285
11	32.4	95.3	135	9 CG529677	CG529677 OST164977
12	32.4	95.3	139	9 CG495088	CG495088 OST34325
13	32.4	95.3	140	9 CG667250	CG667250 OST459771
14	32.4	95.3	146	9 CG589974	CG589974 OST242842
15	32.4	95.3	151	9 CG666807	CG666807 OST457802
16	32.4	95.3	153	9 CG523992	CG523992 OST97396
17	32.4	95.3	161	9 CG609937	CG609937 OST291997
18	32.4	95.3	162	9 CG536645	CG536645 OST124810
19	32.4	95.3	168	9 CG523685	CG523685 OST110501
20	32.4	95.3	175	9 CR202574	CR202574 Forward s
21	32.4	95.3	182	9 CG522772	CG522772 OST92942
22	32.4	95.3	182	9 CG526410	CG526410 OST102968
23	32.4	95.3	189	9 CG528753	CG528753 OST108468
24	32.4	95.3	194	9 CG671483	CG671483 OST500326

c 25	32.4	95.3	206	9 CG668768	CG668768 OST465032
c 26	32.4	95.3	208	9 CR069250	CR069250 Forward s
c 27	32.4	95.3	216	9 CG573772	CG573772 OST205796
c 28	32.4	95.3	216	9 CG579328	CG579328 OST217546
c 29	32.4	95.3	219	9 CG667178	CG667178 OST459480
c 30	32.4	95.3	222	9 CR271082	CR271082 Forward s
c 31	32.4	95.3	228	9 CG669744	CG669744 OST466974
c 32	32.4	95.3	239	9 CG667464	CG667464 OST460949
c 33	32.4	95.3	241	9 CG670326	CG670326 OST467977
c 34	32.4	95.3	253	9 CG527478	CG527478 OST105467
c 35	32.4	95.3	254	9 CG667921	CG667921 OST462816
c 36	32.4	95.3	279	9 CG670404	CG670404 OST470227
c 37	32.4	95.3	280	9 CG545746	CG545746 OST144318
c 38	32.4	95.3	281	9 CG667916	CG667916 OST462797
c 39	32.4	95.3	285	9 CG666517	CG666517 OST456648
c 40	32.4	95.3	285	9 CG666761	CG666761 OST457607
c 41	32.4	95.3	293	9 CG666889	CG666889 OST458215
c 42	32.4	95.3	306	9 CG666905	CG666905 OST458288
c 43	32.4	95.3	314	9 CG557567	CG557567 OST174044
c 44	32.4	95.3	314	9 CG668319	CG668319 OST464162
c 45	32.4	95.3	316	9 CG667495	CG667495 OST461130

ALIGNMENTS

RESULT 1
CG654127/c
LOCUS OST420864 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST420864,
DEFINITION mRNA sequence.
ACCESSION CG654127
VERSION CG654127.1 GI:37477976
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 74)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparkes, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wki kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

TITLE Wki kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene trap.
Location/Qualifiers

source 1. 74
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST420864"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
Query Match 95.3%; Score 32.4; DB 9; Length 74;
Best Local Similarity 97.1%; Pred. No. 0.0086;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GAAGTTCTATCTTCTGGAGATAGGAATTC 34

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 15:17:50 ; Search time 306.75 Seconds
(without alignments)
718.497 Million cell updates/sec

Title: US-10-089-380-5

Perfect score: 34

Sequence: 1 gaggtctctatacttctggagaataggacttc 34

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	32.4	95.3	34	8	US-08-866-279A-14
C 2	32.4	95.3	34	9	US-09-920-932-2
C 3	32.4	95.3	34	9	US-09-804-653-7
C 4	32.4	95.3	34	9	US-09-748-739A-24
C 5	32.4	95.3	34	9	US-09-822-634-18
C 6	32.4	95.3	34	10	US-09-948-193-5
C 7	32.4	95.3	34	10	US-09-997-209-90

C 8	32.4	95.3	34	13	US-10-086-542A-3
C 9	32.4	95.3	34	15	US-10-005-602-5
C 10	32.4	95.3	34	15	US-10-353-445-10
C 11	32.4	95.3	34	16	US-10-368-442-7
C 12	32.4	95.3	34	17	US-10-430-907-1
C 13	32.4	95.3	34	17	US-10-430-908-1
C 14	32.4	95.3	34	17	US-10-440-030-1
C 15	32.4	95.3	34	17	US-10-378-064-4
C 16	32.4	95.3	34	17	US-10-444-664-3
C 17	32.4	95.3	34	18	US-10-639-751-1
C 18	32.4	95.3	34	18	US-10-433-206-90
C 19	32.4	95.3	34	19	US-10-849-547-19
C 20	32.4	95.3	34	20	US-10-623-386-18
C 21	32.4	95.3	34	20	US-10-846-700-14
C 22	32.4	95.3	34	21	US-10-469-508-44
C 23	32.4	95.3	34	21	US-10-976-042-39
C 24	32.4	95.3	34	22	US-10-954-721-18
C 25	32.4	95.3	42	10	US-09-843-150-24
C 26	32.4	95.3	42	10	US-09-843-150-25
C 27	32.4	95.3	42	18	US-10-370-176-55
C 28	32.4	95.3	42	20	US-10-475-962-24
C 29	32.4	95.3	42	20	US-10-475-962-25
C 30	32.4	95.3	48	8	US-08-866-279A-15
C 31	32.4	95.3	48	9	US-09-351-819-2
C 32	32.4	95.3	48	15	US-10-206-163-2
C 33	32.4	95.3	48	15	US-10-161-403-62
C 34	32.4	95.3	48	15	US-10-161-403-63
C 35	32.4	95.3	48	16	US-10-252-279-3
C 36	32.4	95.3	48	20	US-10-846-700-15
C 37	32.4	95.3	54	8	US-08-866-279A-3
C 38	32.4	95.3	54	20	US-10-846-700-3
C 39	32.4	95.3	58	10	US-09-843-150-32
C 40	32.4	95.3	58	10	US-09-843-150-33
C 41	32.4	95.3	58	16	US-10-182-616-29
C 42	32.4	95.3	58	16	US-10-182-616-30
C 43	32.4	95.3	58	20	US-10-475-962-32
C 44	32.4	95.3	58	20	US-10-475-962-33
C 45	32.4	95.3	59	8	US-08-866-279A-2

ALIGNMENTS

RESULT 1

US-08-866-279A-14/c
; Sequence 14, Application US/08866279A
; Publication No. US20020170076A1
; GENERAL INFORMATION:
; APPLICANT: Susan DYMECKI
; TITLE OF INVENTION: Use of Flp Recombinase in Mice
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,279A
; FILING DATE: 30-MAY-1997
; CLASSIFICATION: 800
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 13:28:42 ; Search time 59.5 Seconds
(without alignments)
935.015 Million cell updates/sec

Title: US-10-089-380-5

Perfect score: 34

Sequence: 1 gaagttctatacttcttggaataggaaattc 34

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfilesi.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	32.4	95.3	34	1	US-08-484-324-3
C 2	32.4	95.3	34	1	US-08-486-409-3
C 3	32.4	95.3	34	2	US-08-864-224-18
C 4	32.4	95.3	34	2	US-08-975-763-3
C 5	32.4	95.3	34	2	US-08-825-784-3
C 6	32.4	95.3	34	2	US-08-972-258-4
C 7	32.4	95.3	34	3	US-09-011-257-2
C 8	32.4	95.3	34	3	US-08-745-404-5
C 9	32.4	95.3	34	3	US-09-263-128-4
C 10	32.4	95.3	34	3	US-09-193-502-1
C 11	32.4	95.3	34	3	US-09-193-503B-10
C 12	32.4	95.3	34	3	US-09-193-473-3
C 13	32.4	95.3	34	3	US-09-193-484-1
C 14	32.4	95.3	34	3	US-09-563-233-2
C 15	32.4	95.3	34	3	US-09-438-874A-1
C 16	32.4	95.3	34	3	US-09-439-158-1
C 17	32.4	95.3	34	4	US-09-415-839-10
C 18	32.4	95.3	34	4	US-09-718-034-1
C 19	32.4	95.3	34	4	US-09-606-323C-4
C 20	32.4	95.3	34	4	US-09-438-239-1
C 21	32.4	95.3	34	4	US-09-439-042A-1
C 22	32.4	95.3	34	4	US-09-455-050A-1
C 23	32.4	95.3	34	4	US-09-411-828-3
C 24	32.4	95.3	34	4	US-09-793-372-19
C 25	32.4	95.3	34	4	US-09-641-111A-4
C 26	32.4	95.3	34	4	US-09-869-185B-1
C 27	32.4	95.3	34	4	US-09-937-837-8

C 28	32.4	95.3	34	4	US-08-866-279A-14	Sequence 14, Appl
C 29	32.4	95.3	34	4	US-09-122-384-18	Sequence 18, Appl
C 30	32.4	95.3	34	5	PCT-US92-01899-3	Sequence 3, Appl
C 31	32.4	95.3	36	4	US-09-869-185B-14	Sequence 11, Appl
C 32	32.4	95.3	40	4	US-09-869-185B-11	Sequence 14, Appl
C 33	32.4	95.3	40	4	US-09-869-185B-12	Sequence 12, Appl
C 34	32.4	95.3	44	4	US-09-869-185B-13	Sequence 13, Appl
C 35	32.4	95.3	48	4	US-08-866-279A-15	Sequence 15, Appl
C 36	32.4	95.3	51	3	US-09-837-863-3	Sequence 3, Appl
C 37	32.4	95.3	51	3	US-09-837-863-4	Sequence 4, Appl
C 38	32.4	95.3	52	3	US-09-837-863-11	Sequence 11, Appl
C 39	32.4	95.3	52	3	US-09-837-863-12	Sequence 12, Appl
C 40	32.4	95.3	53	3	US-09-837-863-5	Sequence 5, Appl
C 41	32.4	95.3	53	3	US-09-837-863-6	Sequence 6, Appl
C 42	32.4	95.3	54	1	US-08-010-997-9	Sequence 9, Appl
C 43	32.4	95.3	54	1	US-08-612-551-9	Sequence 9, Appl
C 44	32.4	95.3	54	2	US-09-006-232-9	Sequence 9, Appl
C 45	32.4	95.3	54	3	US-09-211-408-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-08-484-324-3/c

; Sequence 3, Application US/08484324

; Patent No. 5654182

; GENERAL INFORMATION:

; APPLICANT: Wahl, Geoffrey M

; APPLICANT: O'Gorman, Stephen V

; TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN

; TITLE OF INVENTION: MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL

; TITLE OF INVENTION: THEREFOR

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

; STREET: 444 South Flower Street, Suite 2000

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/484,324

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Reiter, Stephen E

; REGISTRATION NUMBER: 31,192

; REFERENCE/DOCKET NUMBER: P41 9984

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 546-4737

; TELEFAX: (619) 546-9392

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-484-324-3

Query Match 95.3%; Score 32.4; DB 1; Length 34;

Best Local Similarity 97.1%; Pred. No. 6.4e-05;

Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGTTCCTACTTCTTCTGGAGAAATAGGAATTC 34

Db 34 GAAGTTCCTACTTCTTCTAGAGAAATAGGAATTC 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 10:55:04 ; Search time 199 Seconds

(without alignments)

1011.413 Million cell updates/sec

Title: US-10-089-380-5

Perfect score: 34

Sequence: 1 gaagttccatacttcttgagaataggaaacttc 34

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002as:*

7: Geneseq2002bs:*

8: Geneseq2003as:*

9: Geneseq2003bs:*

10: Geneseq2003cs:*

11: Geneseq2003ds:*

12: Geneseq2004as:*

13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	34	AAF87359	Aaf87359 Yeast FRT
2	34	100.0	52	AAF87369	Aaf87369 Mutant FR
3	34	100.0	52	AAF87378	Aaf87378 Mutant FR
4	32.4	95.3	34	AAT92196	Aat92196 S. cerevi
5	32.4	95.3	34	AAT92196	Aat92196 S. cerevi
6	32.4	95.3	34	AAV43562	AAV43562 FLP recom
7	32.4	95.3	34	AAV61227	AAV61227 Wild type
8	32.4	95.3	34	AAV72331	AAV72331 Wild type
9	32.4	95.3	34	AAV72331	AAV72331 Wild type
10	32.4	95.3	34	AAV72331	AAV72331 Wild type
11	32.4	95.3	34	AAV72331	AAV72331 Wild type
12	32.4	95.3	34	AAV72331	AAV72331 Wild type
13	32.4	95.3	34	AAV72331	AAV72331 Wild type
14	32.4	95.3	34	AAV72331	AAV72331 Wild type
15	32.4	95.3	34	AAV72331	AAV72331 Wild type
16	32.4	95.3	34	AAV72331	AAV72331 Wild type
17	32.4	95.3	34	AAV72331	AAV72331 Wild type
18	32.4	95.3	34	AAV72331	AAV72331 Wild type
19	32.4	95.3	34	AAV72331	AAV72331 Wild type
20	32.4	95.3	34	AAV72331	AAV72331 Wild type

C 21	32.4	95.3	34	6	AA46212	Yeast FRT
C 22	32.4	95.3	34	6	AA46212	Yeast FRT
C 23	32.4	95.3	34	6	AA46212	Yeast FRT
C 24	32.4	95.3	34	6	AA46212	Yeast FRT
C 25	32.4	95.3	34	6	AA46212	Yeast FRT
C 26	32.4	95.3	34	6	AA46212	Yeast FRT
C 27	32.4	95.3	34	6	AA46212	Yeast FRT
C 28	32.4	95.3	34	6	AA46212	Yeast FRT
C 29	32.4	95.3	34	6	AA46212	Yeast FRT
C 30	32.4	95.3	34	6	AA46212	Yeast FRT
C 31	32.4	95.3	34	6	AA46212	Yeast FRT
C 32	32.4	95.3	34	6	AA46212	Yeast FRT
C 33	32.4	95.3	34	6	AA46212	Yeast FRT
C 34	32.4	95.3	34	6	AA46212	Yeast FRT
C 35	32.4	95.3	34	6	AA46212	Yeast FRT
C 36	32.4	95.3	34	6	AA46212	Yeast FRT
C 37	32.4	95.3	34	6	AA46212	Yeast FRT
C 38	32.4	95.3	34	6	AA46212	Yeast FRT
C 39	32.4	95.3	34	6	AA46212	Yeast FRT
C 40	32.4	95.3	34	6	AA46212	Yeast FRT
C 41	32.4	95.3	34	6	AA46212	Yeast FRT
C 42	32.4	95.3	34	6	AA46212	Yeast FRT
C 43	32.4	95.3	34	6	AA46212	Yeast FRT
C 44	32.4	95.3	34	6	AA46212	Yeast FRT
C 45	32.4	95.3	34	6	AA46212	Yeast FRT

ALIGNMENTS

RESULT 1
AAF87359
ID AAF87359 standard; DNA; 34 BP.
XX
AC AAF87359;
XX
DT 09-JUL-2001 (first entry)
XX
DE Yeast FRT sequence variant #4.
XX
KW Yeast; FRT; gene therapy; gene insertion; gene replacement;
KW DNA recombination; recombinase; FLP; transgenic animal; variant; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200123545-A1.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-JP006686.
XX
PR 30-SEP-1999; 99JP-00280210.
PR 06-DEC-1999; 99JP-00346727.
XX
(SUMU) SUMITOMO PHARM CO LTD.
(SAIT/) SAITO I.
Saito I, Kanegae Y;
WPI, 2001-266149/27.
Variant FRT sequences useful for in vivo gene therapy comprises central 8 base spacer sequence.
Disclosure; Page 58; 73pp; Japanese.

The present sequence is a variant of the FRT sequence from Saccharomyces cerevisiae. Variant FRT sequences may be used in a method of performing highly efficient gene insertion or gene replacement. The variant FRT sequences each undergo a recombination reaction with another variant FRT of the same sequence in the presence of recombinase FLP. The method is useful for producing transgenic animal cells and animals. By locally inserting the DNA and recombinase FLP, genes can be targeted to specific

Result No.	Score	Query Match	Length	DB	ID	Description
1	34	100.0	34	6	BD013288	BD013288 DNA compr
2	34	100.0	52	6	BD013298	BD013298 DNA compr
C 3	34	100.0	52	6	BD013307	BD013307 DNA compr
4	32.4	95.3	34	6	A59775	A59775 Sequence 2
C 5	32.4	95.3	34	6	AR067801	AR067801 Sequence
C 6	32.4	95.3	34	6	AR105498	AR105498 Sequence
C 7	32.4	95.3	34	6	AR130339	AR130339 Sequence
C 8	32.4	95.3	34	6	AR142481	AR142481 Sequence
C 9	32.4	95.3	34	6	BD246903	BD246903 Improved
C 10	32.4	95.3	34	6	BD267670	BD267670 Delivery
11	32.4	95.3	34	6	CQ819068	CQ819068 Sequence
12	32.4	95.3	34	6	E43464	E43464 Method for
C 13	32.4	95.3	34	6	I59685	I59685 Sequence 3
C 14	32.4	95.3	34	6	I69353	I69353 Sequence 3
15	32.4	95.3	34	6	AR194975	AR194975 Sequence
C 16	32.4	95.3	34	6	AR223295	AR223295 Sequence
C 17	32.4	95.3	34	6	AR234678	AR234678 Sequence
C 18	32.4	95.3	34	6	AR264370	AR264370 Sequence
C 19	32.4	95.3	34	6	AR302446	AR302446 Sequence

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 12:20:40 ; Search time 1692 seconds
(without alignments)
764.885 Million cell updates/sec

Title: US-10-089-380-4

Perfect score: 34

Sequence: 1 gaagttctactatcttgagaataggaaacttc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_hcc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	30.8	90.6	74	9	CG654127 OST420864
C 2	30.8	90.6	81	1	A1265023
C 3	30.8	90.6	81	1	A1265111
C 4	30.8	90.6	81	1	A1272501
C 5	30.8	90.6	88	1	A1316311
C 6	30.8	90.6	106	9	CG548652 OST150646
C 7	30.8	90.6	112	9	CG606396
C 8	30.8	90.6	124	9	CG529627 OST110354
C 9	30.8	90.6	130	9	CG526837 OST103896
C 10	30.8	90.6	133	9	CG529602 OST110285
C 11	30.8	90.6	135	9	CG552967 OST164977
C 12	30.8	90.6	139	9	CG495088 OST14325
C 13	30.8	90.6	140	9	CG667250 OST459771
C 14	30.8	90.6	146	9	CG589974 OST424842
C 15	30.8	90.6	151	9	CG666807 OST457802
C 16	30.8	90.6	153	9	CG523992 OST97396
C 17	30.8	90.6	161	9	CG609937 OST291997
C 18	30.8	90.6	162	9	CG536645 OST124810
C 19	30.8	90.6	168	9	CG529685 OST110501
C 20	30.8	90.6	175	9	CR202574 Forward s
C 21	30.8	90.6	182	9	CG522772 OST92942
C 22	30.8	90.6	182	9	CG526410 OST102968
C 23	30.8	90.6	189	9	CG528753 OST108468
C 24	30.8	90.6	194	9	CG671483 OST500326

C 25	30.8	90.6	206	9	CG668768
C 26	30.8	90.6	208	9	CR069250 Forward s
C 27	30.8	90.6	216	9	CG573772 OST205796
C 28	30.8	90.6	216	9	CG579328 OST217546
C 29	30.8	90.6	219	9	CG667178 OST459480
C 30	30.8	90.6	222	9	CR271082 Forward s
C 31	30.8	90.6	228	9	CG669744 OST466974
C 32	30.8	90.6	239	9	CG667464 OST460949
C 33	30.8	90.6	241	9	CG670326 OST469797
C 34	30.8	90.6	253	9	CG527478 OST105467
C 35	30.8	90.6	254	9	CG667921 OST462816
C 36	30.8	90.6	279	9	CG670404 OST470227
C 37	30.8	90.6	280	9	CG545746 OST144318
C 38	30.8	90.6	281	9	CG667916 OST462797
C 39	30.8	90.6	285	9	CG666517 OST456648
C 40	30.8	90.6	285	9	CG666761 OST457607
C 41	30.8	90.6	293	9	CG666889 OST458215
C 42	30.8	90.6	306	9	CG666905 OST458288
C 43	30.8	90.6	314	9	CG557567 OST174044
C 44	30.8	90.6	314	9	CG668319 OST464162
C 45	30.8	90.6	316	9	CG667495 OST461130

ALIGNMENTS

RESULT 1
CG654127/c

LOCUS

DEFINITION

CG654127

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 74

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129Sv/Ev"

/db_xref="taxon:10090"

/clone="OST420864"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match

Best Local Similarity

Matches

32; Conservative

0; Mismatches

2; Indels

0; Gaps

0; Length

74;

Score 30.8;

Pred. No. 0.051;

1 GAAGTTCTACTATCTTGAGAACTTC 34

CG654127

OST420864

Mus musculus

musculus

musculus

musculus

musculus

musculus

musculus

musculus

musculus

musculus

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 15:17:50 ; Search time 306.75 Seconds
(without alignments)
718.497 Million cell updates/sec

Title: US-10-089-380-4
Perfect score: 34
Sequence: 1 gaagttctatactattctgagaatgaacttc 34

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
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- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	30.8	90.6	34	8	US-08-866-279A-14
C 2	30.8	90.6	34	9	US-09-920-932-2
C 3	30.8	90.6	34	9	US-09-804-653-7
C 4	30.8	90.6	34	9	US-09-748-739A-24
C 5	30.8	90.6	34	9	US-09-822-634-18
C 6	30.8	90.6	34	10	US-09-948-193-5
C 7	30.8	90.6	34	10	US-09-997-209-90

C 8	30.8	90.6	34	13	US-10-086-542A-3
C 9	30.8	90.6	34	15	US-10-005-602-5
C 10	30.8	90.6	34	15	US-10-353-445-10
C 11	30.8	90.6	34	16	US-10-368-442-7
C 12	30.8	90.6	34	17	US-10-430-907-1
C 13	30.8	90.6	34	17	US-10-430-908-1
C 14	30.8	90.6	34	17	US-10-440-030-1
C 15	30.8	90.6	34	17	US-10-378-064-4
C 16	30.8	90.6	34	17	US-10-444-664-3
C 17	30.8	90.6	34	18	US-10-639-751-1
C 18	30.8	90.6	34	18	US-10-433-206-90
C 19	30.8	90.6	34	19	US-10-649-547-19
C 20	30.8	90.6	34	20	US-10-623-386-18
C 21	30.8	90.6	34	20	US-10-846-700-14
C 22	30.8	90.6	34	21	US-10-469-508-44
C 23	30.8	90.6	34	21	US-10-976-042-39
C 24	30.8	90.6	34	22	US-10-954-721-18
C 25	30.8	90.6	42	10	US-09-843-150-24
C 26	30.8	90.6	42	10	US-09-843-150-25
C 27	30.8	90.6	42	18	US-10-270-176-55
C 28	30.8	90.6	42	20	US-10-475-962-24
C 29	30.8	90.6	42	20	US-10-475-962-25
C 30	30.8	90.6	48	8	US-08-866-279A-15
C 31	30.8	90.6	48	9	US-09-351-819-2
C 32	30.8	90.6	48	15	US-10-206-163-2
C 33	30.8	90.6	48	15	US-10-161-403-62
C 34	30.8	90.6	48	15	US-10-161-403-63
C 35	30.8	90.6	48	16	US-10-252-279-3
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C 37	30.8	90.6	54	8	US-08-866-279A-3
C 38	30.8	90.6	54	20	US-10-846-700-3
C 39	30.8	90.6	58	10	US-09-843-150-32
C 40	30.8	90.6	58	10	US-09-843-150-33
C 41	30.8	90.6	58	16	US-10-182-616-29
C 42	30.8	90.6	58	16	US-10-182-616-30
C 43	30.8	90.6	58	20	US-10-475-962-32
C 44	30.8	90.6	58	20	US-10-475-962-33
C 45	30.8	90.6	59	8	US-08-866-279A-2

ALIGNMENTS

RESULT 1
US-08-866-279A-14/c
; Sequence 14, Application US/08866279A
; Publication No. US20020170076A1
; GENERAL INFORMATION:
; APPLICANT: Susan DYMECKI
; TITLE OF INVENTION: Use of Flp Recombinase in Mice
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866, 279A
; FILING DATE: 30-MAY-1997
; CLASSIFICATION: 800
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 13:28:42 ; Search time 59.5 Seconds
(without alignments)
935.015 Million cell updates/sec

Title: US-10-089-380-4

Perfect score: 34

Sequence: 1 gaagttcctatactatcttgagaataggaaattc 34

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/prodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PCTUS COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	30.8	90.6	34	1	US-08-484-324-3
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C 4	30.8	90.6	34	2	US-08-975-763-3
C 5	30.8	90.6	34	2	US-08-925-784-3
C 6	30.8	90.6	34	2	US-08-972-258-4
C 7	30.8	90.6	34	3	US-09-011-257-2
C 8	30.8	90.6	34	3	US-08-745-404-5
C 9	30.8	90.6	34	3	US-09-263-128-4
C 10	30.8	90.6	34	3	US-09-193-502-1
C 11	30.8	90.6	34	3	US-09-193-503B-10
C 12	30.8	90.6	34	3	US-09-193-475-3
C 13	30.8	90.6	34	3	US-09-193-484-1
C 14	30.8	90.6	34	3	US-09-563-239-2
C 15	30.8	90.6	34	3	US-09-438-874A-1
C 16	30.8	90.6	34	3	US-09-439-158-1
C 17	30.8	90.6	34	4	US-09-415-839-10
C 18	30.8	90.6	34	4	US-09-718-034-1
C 19	30.8	90.6	34	4	US-09-606-323C-4
C 20	30.8	90.6	34	4	US-09-438-239-1
C 21	30.8	90.6	34	4	US-09-439-042A-1
C 22	30.8	90.6	34	4	US-09-455-050A-1
C 23	30.8	90.6	34	4	US-09-411-826-3
C 24	30.8	90.6	34	4	US-09-793-372-19
C 25	30.8	90.6	34	4	US-09-641-111A-4
C 26	30.8	90.6	34	4	US-09-869-185B-1
C 27	30.8	90.6	34	4	US-09-937-837-8

C 28	30.8	90.6	34	4	US-08-866-279A-14	Sequence 14, Appl
C 29	30.8	90.6	34	4	US-09-122-384-18	Sequence 18, Appl
C 30	30.8	90.6	34	5	PCT-US92-01899-3	Sequence 3, Appl
C 31	30.8	90.6	36	4	US-09-869-185B-14	Sequence 14, Appl
C 32	30.8	90.6	40	4	US-09-869-185B-11	Sequence 11, Appl
C 33	30.8	90.6	40	4	US-09-869-185B-12	Sequence 12, Appl
C 34	30.8	90.6	44	4	US-08-866-279A-15	Sequence 15, Appl
C 35	30.8	90.6	48	4	US-08-866-279A-15	Sequence 15, Appl
C 36	30.8	90.6	51	3	US-09-837-863-3	Sequence 4, Appl
C 37	30.8	90.6	51	3	US-09-837-863-4	Sequence 4, Appl
C 38	30.8	90.6	52	3	US-09-837-863-11	Sequence 11, Appl
C 39	30.8	90.6	52	3	US-09-837-863-12	Sequence 12, Appl
C 40	30.8	90.6	53	3	US-09-837-863-5	Sequence 5, Appl
C 41	30.8	90.6	53	3	US-09-837-863-6	Sequence 6, Appl
C 42	30.8	90.6	54	1	US-08-010-997-9	Sequence 9, Appl
C 43	30.8	90.6	54	1	US-08-612-551-9	Sequence 9, Appl
C 44	30.8	90.6	54	2	US-09-006-232-9	Sequence 9, Appl
C 45	30.8	90.6	54	3	US-09-211-408-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-08-484-324-3/c

; Sequence 3, Application US/08484324

; Patent No. 5654182

; GENERAL INFORMATION:

; APPLICANT: Wahl, Geoffrey M

; TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN

; TITLE OF INVENTION: MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

; STREET: 444 South Flower Street, Suite 2000

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/484,324

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Reiter, Stephen E

; REGISTRATION NUMBER: 31,192

; REFERENCE/DOCKET NUMBER: P41 9984

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 546-4737

; TELEFAX: (619) 546-9392

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-484-324-3

Query Match 90.6%; Score 30.8; DB 1; Length 34;

Best Local Similarity 94.1%; Pred. No. 0.00062;

Mismatches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAGTTCCTATACTATCTTGAGAATAGGAATTC 34

DB 34 GAAGTTCCTATACTATCTTGAGAATAGGAATTC 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 10:55:04 ; Search time 199 Seconds
(without alignments)
1011.413 Million cell updates/sec

Title: US-10-089-380-4

Perfect score: 34

Sequence: 1 gaagtctctatactatcttgagaataggaacttc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002as.*
- 7: Geneseq2002bs.*
- 8: Geneseq2003as.*
- 9: Geneseq2003bs.*
- 10: Geneseq2003cs.*
- 11: Geneseq2003ds.*
- 12: Geneseq2004as.*
- 13: Geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	34	4	Aaf87358 Yeast FRT
2	34	100.0	52	4	Aaf87384 Mutant FR
3	34	100.0	52	4	Aaf87375 Mutant FR
4	32.4	95.3	34	3	Aac63092 Mutant FR
5	32.4	95.3	50	6	Aba97763 Oligonucle
6	32.4	95.3	52	4	Aaf87368 Mutant FR
7	32.4	95.3	52	4	Aaf87377 Mutant FR
8	32.4	95.3	58	6	Aba97761 Oligonucle
9	32.4	95.3	60	6	Aba97762 Oligonucle
10	32.4	95.3	1359	9	ACC85347 PC8199-3
11	32.4	95.3	1359	10	Ade34325 Plastid t
12	32.4	95.3	2077	9	ACC85385 Vector pC
13	32.4	95.3	2662	9	ACC85386 Vector pC
14	30.8	90.6	34	2	Aat92196 S. cerevi
15	30.8	90.6	34	2	Aav43562 FLP recom
16	30.8	90.6	34	2	Aax61227 Wild type
17	30.8	90.6	34	2	Aav72331 Wild type
18	30.8	90.6	34	2	Aax01426 2mu FRT e
19	30.8	90.6	34	2	Aai72854 Minimal F
20	30.8	90.6	34	3	Aaz58072 FLP recom

C 21	30.8	90.6	34	3	AAC61513	Aac61513 Nucleotid
C 22	30.8	90.6	34	3	AAA10237	Aaa10237 FLP recom
C 23	30.8	90.6	34	3	AAC63090	Aac63090 Wild-type
C 24	30.8	90.6	34	4	AAF24488	Aaf24488 FLP recom
C 25	30.8	90.6	34	4	AAD10220	Aad10220 Minimal w
C 26	30.8	90.6	34	4	AAF81218	Aaf81218 FLP recom
27	30.8	90.6	34	4	AAF87356	Aaf87356 Yeast FRT
28	30.8	90.6	34	4	AAF87359	Aaf87359 Yeast FRT
29	30.8	90.6	34	4	AAF87362	Aaf87362 Yeast FRT
30	30.8	90.6	34	4	AAF87355	Aaf87355 Yeast FRT
31	30.8	90.6	34	4	AAB21799	Aab21799 Saccharom
32	30.8	90.6	34	5	AAS14781	Aas14781 FLP recom
C 33	30.8	90.6	34	6	AAD46212	Aad46212 Yeast FRT
C 34	30.8	90.6	34	6	AAD24140	Aad24140 Recombina
C 35	30.8	90.6	34	6	AAD35275	Aad35275 FRT recog
C 36	30.8	90.6	34	6	ABA03777	Aba03777 Saccharom
C 37	30.8	90.6	34	6	AAD41158	Aad41158 Yeast tar
C 38	30.8	90.6	34	6	AAL49298	Aal49298 FLP recom
C 39	30.8	90.6	34	7	ADL18609	Adl18609 FRT site
C 40	30.8	90.6	34	8	ABX13963	Abx13963 Yeast FLP
41	30.8	90.6	34	8	ADA88940	Ada88940 FLP recog
C 42	30.8	90.6	34	8	ABX93111	Abx93111 Minimal F
C 43	30.8	90.6	34	9	ACC85315	Acc85315 Recombina
C 44	30.8	90.6	34	9	ACD26382	Acd26382 FRT recom
C 45	30.8	90.6	34	10	ADC17306	Adc17306 Baker's y

ALIGNMENTS

RESULT 1

AAF87358
ID AAF87358 standard; DNA; 34 BP.
XX
AC AAF87358;
XX
DT 09-JUL-2001 (first entry)
XX
DE Yeast FRT sequence variant #3.
XX
KW Yeast; FRT; gene therapy; gene insertion; gene replacement;
KW DNA recombination; recombinase; FLP; transgenic animal; variant; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WC200123545-A1.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-JP006686.
XX
PR 30-SEP-1999; 99JP-00280210.
PR 06-DEC-1999; 99JP-00346727.
XX
(SUMU) SUMITOMO PHARM CO LTD.
(SAIT/) SAITO I.
PI Saito I, Kanegae Y;
DR WPI; 2001-266149/27.
XX
PT Variant FRT sequences useful for in vivo gene therapy comprises central 8
base spacer sequence.
XX
PS Disclosure; Page 57; 73pp; Japanese.
XX
CC The present sequence is a variant of the FRT sequence from Saccharomyces
cerevisiae. Variant FRT sequences may be used in a method of performing
highly efficient gene insertion or gene replacement. The variant FRT
sequences each undergo a recombination reaction with another variant FRT
of the same sequence in the presence of recombinase FLP. The method is
useful for producing transgenic animal cells and animals. By locally
inserting the DNA and recombinase FLP, genes can be targeted to specific

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 10:58:49 ; Search time 741.75 Seconds
(without alignments)
2221.068 Million cell updates/sec

Title: US-10-089-380-4

Perfect score: 34

Sequence: 1 gaagtcctatactattgagaataggaaattc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_st.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	34	6	BD013287
2	34	100.0	52	6	BD013304 DNA compr
3	34	100.0	52	6	BD013313 DNA compr
4	32.4	95.3	52	6	BD013297 DNA compr
5	32.4	95.3	52	6	BD013306 DNA compr
6	32.4	95.3	1359	6	AX798126 Sequence
7	32.4	95.3	1359	6	AX798910 Sequence
8	32.4	95.3	2077	6	AX798172 Sequence
9	32.4	95.3	2662	6	AX798173 Sequence
10	30.8	90.6	34	6	AS9775 Sequence 2
11	30.8	90.6	34	6	AR067801 Sequence
12	30.8	90.6	34	6	AR105498 Sequence
13	30.8	90.6	34	6	AR130339 Sequence
14	30.8	90.6	34	6	AR142481 Sequence
15	30.8	90.6	34	6	BD246903 Improved
16	30.8	90.6	34	6	BD267670 Delivery
17	30.8	90.6	34	6	CQ819068 Sequence
18	30.8	90.6	34	6	E43464 Method for
19	30.8	90.6	34	6	I59685 Sequence 3

C	20	30.8	90.6	34	6	I69353	Sequence 3
	21	30.8	90.6	34	6	AR194975	Sequence
C	22	30.8	90.6	34	6	AR232395	Sequence
C	23	30.8	90.6	34	6	AR234678	Sequence
C	24	30.8	90.6	34	6	AR264370	Sequence
C	25	30.8	90.6	34	6	AR302446	Sequence
C	26	30.8	90.6	34	6	AR302544	Sequence
C	27	30.8	90.6	34	6	AR307970	Sequence
C	28	30.8	90.6	34	6	AR342117	Sequence
C	29	30.8	90.6	34	6	AR370679	Sequence
C	30	30.8	90.6	34	6	AR403690	Sequence
C	31	30.8	90.6	34	6	AR438854	Sequence
C	32	30.8	90.6	34	6	AR477307	Sequence
C	33	30.8	90.6	34	6	AR494802	Sequence
C	34	30.8	90.6	34	6	AR527595	Sequence
C	35	30.8	90.6	34	6	AX101007	Sequence
	36	30.8	90.6	34	6	AX269147	Sequence
C	37	30.8	90.6	34	6	AX359678	Sequence
C	38	30.8	90.6	34	6	AX453121	Sequence
C	39	30.8	90.6	34	6	AX555208	Sequence
	40	30.8	90.6	34	6	AX657059	Sequence
C	41	30.8	90.6	34	6	AX657060	Sequence
	42	30.8	90.6	34	6	BD013284	DNA compr
C	43	30.8	90.6	34	6	BD013285	DNA compr
	44	30.8	90.6	34	6	BD013288	DNA compr
C	45	30.8	90.6	34	6	BD013291	DNA compr

ALIGNMENTS

BD013287 34 bp DNA linear PAT 02-AUG-2002
DNA comprising mutant FRT sequence.

BD013287
BD013287.1 GI:22093476

WO 0123545-A/4.

Saccharomyces cerevisiae (baker's yeast)

Saccharomyces cerevisiae

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

1 (bases 1 to 34)

Saito, I. and Kanegae, Y.

DNA comprising mutant FRT sequence

Patent: WO 0123545-A 4 05-APR-2001;

IZUMU SAITO, SUMITOMO PHARMACEUTICALS CO LTD, YUMI KANEGAE

OS Saccharomyces cerevisiae (yeast)

PN WO 0123545-A/4

PD 05-APR-2001

PF 28-SEP-2000 WO 2000JP006686

PR 30-SEP-1999 JP 99P 280210, 06-DEC-1999 JP 99P 346727 PI

IZUMU SAITO, YUMI KANEGAE

PC C12N15/11, C12N15/10, A01K67/027, A61K48/00

CC DNA comprising mutant FRT sequence

PH Key Location/Qualifiers

FT source 1..34

FT Location/Qualifiers

/organism='Saccharomyces cerevisiae (yeast)'

source

1..34

/organism='Saccharomyces cerevisiae'

/mol_type='genomic DNA'

/db_xref='taxon:4932'

ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 34;

Best Local Similarity 100.0%; Pred. No. 0.0079;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GAAGTTCCTATCTATCTTGAAGTAAGGAATTC 34

Db 1 GAAGTTCCTATCTATCTTGAAGTAAGGAATTC 34

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 12:20:40 ; Search time 1692 Seconds
(without alignments)
764.885 Million cell updates/sec

Title: US-10-089-380-3

Perfect score: 34

Sequence: 1 gaagttcctatactccagagaataggaaacttc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	30.8	90.6	74	9	CG654127 OST420864
C 2	30.8	90.6	81	1	AI265023 uk01f07.y
C 3	30.8	90.6	81	1	AI265111 uk03c08.y
C 4	30.8	90.6	81	1	AI272501 uk04g01.y
C 5	30.8	90.6	88	1	AI316311 u99a11.y
C 6	30.8	90.6	106	9	CG548652 OST150646
C 7	30.8	90.6	112	9	CG506396 OST284215
C 8	30.8	90.6	124	9	CG529627 OST110354
C 9	30.8	90.6	130	9	CG526837 OST103896
C 10	30.8	90.6	133	9	CG529602 OST110285
C 11	30.8	90.6	135	9	CG52967 OST164977
C 12	30.8	90.6	139	9	CG495088 OST34325
C 13	30.8	90.6	140	9	CG667250 OST459771
C 14	30.8	90.6	146	9	CG589974 OST242842
C 15	30.8	90.6	151	9	CG666807 OST457802
C 16	30.8	90.6	153	9	CG523992 OST97396
C 17	30.8	90.6	161	9	CG609937 OST291997
C 18	30.8	90.6	162	9	CG536645 OST124810
C 19	30.8	90.6	168	9	CG529685 OST110501
C 20	30.8	90.6	175	9	CR202574 Forward s
C 21	30.8	90.6	182	9	CG522772 OST92942
C 22	30.8	90.6	182	9	CG526410 OST102968
C 23	30.8	90.6	189	9	CG528753 OST108468
C 24	30.8	90.6	194	9	CG671483 OST500326

C 25	30.8	90.6	206	9	CG668768
C 26	30.8	90.6	208	9	CR069250
C 27	30.8	90.6	216	9	CG573772
C 28	30.8	90.6	216	9	CG579328
C 29	30.8	90.6	219	9	CG667178
C 30	30.8	90.6	222	9	CR271082
C 31	30.8	90.6	228	9	CG669744
C 32	30.8	90.6	239	9	CG667464
C 33	30.8	90.6	241	9	CG670326
C 34	30.8	90.6	253	9	CG527478
C 35	30.8	90.6	254	9	CG667921
C 36	30.8	90.6	279	9	CG670404
C 37	30.8	90.6	280	9	CG545746
C 38	30.8	90.6	281	9	CG667916
C 39	30.8	90.6	285	9	CG666517
C 40	30.8	90.6	285	9	CG666761
C 41	30.8	90.6	293	9	CG666889
C 42	30.8	90.6	306	9	CG666905
C 43	30.8	90.6	314	9	CG557567
C 44	30.8	90.6	314	9	CG668319
C 45	30.8	90.6	316	9	CG667495

ALIGNMENTS

RESULT 1
LOCUS CG654127/c
DEFINITION CG654127 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST420864, mRNA sequence.
ACCESSION CG654127
VERSION CG654127.1 GI:37477976
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 74)
AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Figgott,J., BeltrandelRio,H., Buxton,E.C., Edwards,D., Finch,R.A., Riddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jiang,C., Key,B.W. Jr., Kipp,P.G., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Slightenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.
TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES
source
1..74
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST420864"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 90.6%; Score 30.8; DB 9; Length 74;
Best Local Similarity 94.1%;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAGTTCTTACTCTCCAGAGATAGGAACCTTC 34

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 15:17:50 ; Search time 306.75 Seconds
(without alignments)
718.497 Million cell updates/sec

Title: US-10-089-380-3

Perfect score: 34

Sequence: 1 gaagttctactctcagagaataggaattc 34

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	30.8	90.6	34	8	US-08-866-279A-14
C 2	30.8	90.6	34	9	US-09-920-932-2
C 3	30.8	90.6	34	9	US-09-804-653-7
C 4	30.8	90.6	34	9	US-09-748-739A-24
C 5	30.8	90.6	34	9	US-09-822-634-18
C 6	30.8	90.6	34	10	US-09-948-193-5
C 7	30.8	90.6	34	10	US-09-997-209-90
C 1	30.8	90.6	34	8	Sequence 14, Appl
C 2	30.8	90.6	34	9	Sequence 2, Appl
C 3	30.8	90.6	34	9	Sequence 7, Appl
C 4	30.8	90.6	34	9	Sequence 24, Appl
C 5	30.8	90.6	34	9	Sequence 18, Appl
C 6	30.8	90.6	34	10	Sequence 5, Appl
C 7	30.8	90.6	34	10	Sequence 90, Appl

ALIGNMENTS

RESULT 1

US-08-866-279A-14/c

; Sequence 14, Application US/08866279A

; Publication No. US0020170076A1

; GENERAL INFORMATION:

; APPLICANT: Susan DYMECKI

; TITLE OF INVENTION: Use of Flp Recombinase in Mice

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.

; STREET: 1100 New York Avenue, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3918

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Microsoft Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/866,279A

; FILING DATE: 30-MAY-1997

; CLASSIFICATION: 800

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

Sequence 3, Appl
Sequence 5, Appl
Sequence 10, Appl
Sequence 7, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 1, Appl
Sequence 90, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 14, Appl
Sequence 44, Appl
Sequence 39, Appl
Sequence 18, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 15, Appl
Sequence 2, Appl
Sequence 62, Appl
Sequence 63, Appl
Sequence 3, Appl
Sequence 15, Appl
Sequence 3, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 2, Appl

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 13:28:42 ; Search time 59.5 seconds
(without alignments)
935.015 Million cell updates/sec

Title: US-10-089-380-3

Perfect score: 34

Sequence: 1 gaagttcttactctccagagaataggaacttc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*

- 1: /cgm2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgm2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgm2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgm2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgm2_6/ptodata/1/ina/PTUS COMB.seq.*
- 6: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	30.8	90.6	34	1	US-08-484-324-3
C 2	30.8	90.6	34	1	US-08-486-409-3
C 3	30.8	90.6	34	2	US-08-864-224-18
C 4	30.8	90.6	34	2	US-08-975-763-3
C 5	30.8	90.6	34	2	US-08-825-784-3
C 6	30.8	90.6	34	2	US-08-972-258-4
C 7	30.8	90.6	34	3	US-09-011-257-2
C 8	30.8	90.6	34	3	US-08-745-404-5
C 9	30.8	90.6	34	3	US-09-263-128-4
C 10	30.8	90.6	34	3	US-09-193-502-1
C 11	30.8	90.6	34	3	US-09-193-503B-10
C 12	30.8	90.6	34	3	US-09-193-475-3
C 13	30.8	90.6	34	3	US-09-193-484-1
C 14	30.8	90.6	34	3	US-09-563-239-2
C 15	30.8	90.6	34	3	US-09-438-874A-1
C 16	30.8	90.6	34	3	US-09-439-158-1
C 17	30.8	90.6	34	4	US-09-415-839-10
C 18	30.8	90.6	34	4	US-09-718-034-1
C 19	30.8	90.6	34	4	US-09-606-323C-4
C 20	30.8	90.6	34	4	US-09-438-239-1
C 21	30.8	90.6	34	4	US-09-439-042A-1
C 22	30.8	90.6	34	4	US-09-455-050A-1
C 23	30.8	90.6	34	4	US-09-411-826-3
C 24	30.8	90.6	34	4	US-09-793-372-19
C 25	30.8	90.6	34	4	US-09-641-111A-4
C 26	30.8	90.6	34	4	US-09-869-185B-1
C 27	30.8	90.6	34	4	US-09-937-837-8

C 28	30.8	90.6	34	4	US-08-866-279A-14	Sequence 14, Appl
C 29	30.8	90.6	34	4	US-09-122-384-18	Sequence 18, Appl
C 30	30.8	90.6	34	5	PCT-US92-01899-3	Sequence 3, Appl
C 31	30.8	90.6	36	4	US-09-869-185B-14	Sequence 14, Appl
C 32	30.8	90.6	40	4	US-09-869-185B-11	Sequence 11, Appl
C 33	30.8	90.6	40	4	US-09-869-185B-12	Sequence 12, Appl
C 34	30.8	90.6	44	4	US-08-866-279A-15	Sequence 15, Appl
C 35	30.8	90.6	48	4	US-09-869-185B-13	Sequence 13, Appl
C 36	30.8	90.6	51	3	US-09-837-863-3	Sequence 3, Appl
C 37	30.8	90.6	51	3	US-09-837-863-4	Sequence 4, Appl
C 38	30.8	90.6	52	3	US-09-837-863-11	Sequence 11, Appl
C 39	30.8	90.6	52	3	US-09-837-863-12	Sequence 12, Appl
C 40	30.8	90.6	53	3	US-09-837-863-5	Sequence 5, Appl
C 41	30.8	90.6	53	3	US-09-837-863-6	Sequence 6, Appl
C 42	30.8	90.6	54	1	US-08-010-997-9	Sequence 9, Appl
C 43	30.8	90.6	54	1	US-08-612-551-9	Sequence 9, Appl
C 44	30.8	90.6	54	2	US-09-006-232-9	Sequence 9, Appl
C 45	30.8	90.6	54	3	US-09-211-408-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-08-484-324-3/c
Sequence 3, Application US/08484324
Patent No. 5654182
GENERAL INFORMATION:
APPLICANT: Wahl, Geoffrey M
TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL THEREFOR
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,324
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9984
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-324-3

Query Match 90.6%; Score 30.8; DB 1; Length 34;
Best Local Similarity 94.1%; Pred. No. 9.4e-05;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAGTTCCTACTCTCCAGAGAAATAGGAACCTC 34
DB 34 GAAGTTCCTACTCTTCTAGAGATAGGAACCTC 1

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 10:55:04 ; Search time 199 Seconds
(without alignments)

1011.413 Million cell updates/sec

Title: US-10-089-380-3

Perfect score: 34

Sequence: 1 gaagttcctatactctccagagaataggaaattc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	34	100.0	52	AAf87374	Aaf87374 Mutant FR
3	34	100.0	52	AAf87383	Aaf87383 Mutant FR
4	30.8	90.6	34	AAT92196	Aat92196 S. cerevi
5	30.8	90.6	34	AAV43562	Aav43562 FLP recom
6	30.8	90.6	34	AAV61227	Aav61227 Wild type
7	30.8	90.6	34	AAV72331	Aav72331 Wild type
8	30.8	90.6	34	AAx01426	Aax01426 2mu FRT e
9	30.8	90.6	34	AAI72854	Aai72854 Minimal F
10	30.8	90.6	34	AAZ58072	Aaz58072 FLP recom
11	30.8	90.6	34	AAc61513	Aac61513 Nucleotid
12	30.8	90.6	34	AAa10237	Aaa10237 FLP recom
13	30.8	90.6	34	AAc63092	Aac63092 Mutant FR
14	30.8	90.6	34	AAc63090	Aac63090 Wild-type
15	30.8	90.6	34	AAf24488	Aaf24488 FLP recom
16	30.8	90.6	34	AAa10220	Aaa10220 Minimal w
17	30.8	90.6	34	AAf81218	Aaf81218 FLP recom
18	30.8	90.6	34	AAf87356	Aaf87356 Yeast FRT
19	30.8	90.6	34	AAf87355	Aaf87355 Yeast FRT
20	30.8	90.6	34	AAh21799	Aah21799 Saccharom

21	30.8	90.6	34	5	AAa14781	AAa14781 FLP recom
22	30.8	90.6	34	6	AAa46212	AAa46212 Yeast FRT
23	30.8	90.6	34	6	AAa24140	AAa24140 Recombina
24	30.8	90.6	34	6	AAa35275	AAa35275 FRT recog
25	30.8	90.6	34	6	AAa03777	AAa03777 Saccharom
26	30.8	90.6	34	6	AAa41158	AAa41158 Yeast tar
27	30.8	90.6	34	6	AAa49298	AAa49298 FLP recom
28	30.8	90.6	34	7	AAa18609	AAa18609 FRT site
29	30.8	90.6	34	8	AAa13963	AAa13963 Yeast FLP
30	30.8	90.6	34	8	AAa88940	AAa88940 FLP recog
31	30.8	90.6	34	8	AAa93111	AAa93111 Minimal F
32	30.8	90.6	34	9	AAc85315	AAc85315 Recombina
33	30.8	90.6	34	9	AAc26382	AAc26382 FRT recom
34	30.8	90.6	34	10	AAc17306	AAc17306 Baker's Y
35	30.8	90.6	34	10	AAa13799	AAa13799 Oligonuc
36	30.8	90.6	34	10	AAa06116	AAa06116 Yeast fli
37	30.8	90.6	34	10	AAa61473	AAa61473 FLP recom
38	30.8	90.6	34	10	AAa81223	AAa81223 FLP recom
39	30.8	90.6	34	10	AAa65708	AAa65708 FLP recog
40	30.8	90.6	34	10	AAa65098	AAa65098 FRT recom
41	30.8	90.6	34	10	AAa08623	AAa08623 Yeast FLP
42	30.8	90.6	34	12	AAa73217	AAa73217 Yeast FLP
43	30.8	90.6	34	12	AAa73015	AAa73015 Yeast FLP
44	30.8	90.6	34	12	AAa126304	AAa126304 FLP recom
45	30.8	90.6	34	12	AAa036182	AAa036182 Non-ident

ALIGNMENTS

RESULT 1
AAf87357
ID AAF87357 standard; DNA; 34 BP.

AC AAF87357;

DT 09-JUL-2001 (first entry)

XX Yeast FRT sequence variant #2.

XX Yeast; FRT; gene therapy; gene insertion; gene replacement;

KW DNA recombination; recombinase; FLP; transgenic animal; variant; ds.

XX Saccharomyces cerevisiae.

XX WO200123545-A1.

XX 05-APR-2001.

XX 28-SEP-2000; 2000WO-JP006686.

XX 30-SEP-1999; 99JP-00280210.

PR 06-DEC-1999; 99JP-00346727.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX (SAIT/) SAITO I.

PI Saito I, Kanegae Y;

XX WPI; 2001-266149/27.

XX Variant FRT sequences useful for in vivo gene therapy comprises central 8

PT base spacer sequence.

XX Disclosure; Page 57; 73pp; Japanese.

XX The present sequence is a variant of the FRT sequence from Saccharomyces

XX cerevisiae. Variant FRT sequences may be used in a method of performing

XX highly efficient gene insertion or gene replacement. The variant FRT

XX sequences each undergo a recombination reaction with another variant FRT

XX of the same sequence in the presence of recombinase FLP. The method is

XX useful for producing transgenic animal cells and animals. By locally

XX inserting the DNA and recombinase FLP, genes can be targeted to specific

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 10:58:49 ; Search time 741.75 Seconds
(without alignments)
2221.068 Million cell updates/sec

Title: US-10-089-380-3
Perfect score: 34
Sequence: 1 gaagttcctatactctccagagaataggaaattc 34

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
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8: gb_pi.*
9: gb_pr.*
10: gb_ro.*
11: gb_scs.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	34	100.0	52	BD013303	BD013303 DNA compr
3	34	100.0	52	BD013312	BD013312 DNA compr
4	30.8	90.6	34	AS9775	AS9775 Sequence 2
5	30.8	90.6	34	AR067801	AR067801 Sequence
6	30.8	90.6	34	AR105498	AR105498 Sequence
7	30.8	90.6	34	AR130339	AR130339 Sequence
8	30.8	90.6	34	AR142481	AR142481 Sequence
9	30.8	90.6	34	BD246903	BD246903 Improved
10	30.8	90.6	34	BD267670	BD267670 Delivery
11	30.8	90.6	34	CQ819068	CQ819068 Sequence
12	30.8	90.6	34	E43464	E43464 Method for
13	30.8	90.6	34	I59685	I59685 Sequence 3
14	30.8	90.6	34	I69353	I69353 Sequence 3
15	30.8	90.6	34	AR194975	AR194975 Sequence
16	30.8	90.6	34	AR232395	AR232395 Sequence
17	30.8	90.6	34	AR234678	AR234678 Sequence
18	30.8	90.6	34	AR264370	AR264370 Sequence
19	30.8	90.6	34	AR302446	AR302446 Sequence

C 20	30.8	90.6	34	6	AR302544	Sequence
C 21	30.8	90.6	34	6	AR307970	Sequence
C 22	30.8	90.6	34	6	AR342117	Sequence
C 23	30.8	90.6	34	6	AR370679	Sequence
C 24	30.8	90.6	34	6	AR403690	Sequence
C 25	30.8	90.6	34	6	AR438854	Sequence
C 26	30.8	90.6	34	6	AR477307	Sequence
C 27	30.8	90.6	34	6	AR494802	Sequence
C 28	30.8	90.6	34	6	AR527595	Sequence
C 29	30.8	90.6	34	6	AX101007	Sequence
C 30	30.8	90.6	34	6	AX269147	Sequence
C 31	30.8	90.6	34	6	AX359678	Sequence
C 32	30.8	90.6	34	6	AX453121	Sequence
C 33	30.8	90.6	34	6	AX555208	Sequence
C 34	30.8	90.6	34	6	AX657059	Sequence
C 35	30.8	90.6	34	6	AX657060	Sequence
C 36	30.8	90.6	34	6	BD013284	DNA compr
C 37	30.8	90.6	34	6	BD013285	DNA compr
C 38	30.8	90.6	34	6	BD083074	Antisense
C 39	30.8	90.6	34	6	BD093613	Antisense
C 40	30.8	90.6	34	6	BD094631	Method fo
C 41	30.8	90.6	35	6	BD271118	Methods f
C 42	30.8	90.6	36	6	E43477	Method for
C 43	30.8	90.6	36	6	AR527608	Sequence
C 44	30.8	90.6	36	6	BD094644	Method fo
C 45	30.8	90.6	39	6	AX377747	Sequence

ALIGNMENTS

RESULT 1
LOCUS BD013286 34 bp DNA linear PAT 02-AUG-2002
DEFINITION DNA comprising mutant FRT sequence.
ACCESSION BD013286
VERSION BD013286.1 GI:22093475
KEYWORDS WO 0123545-A/3.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

REFERENCE 1 (bases 1 to 34)
AUTHORS Saito, I. and Kanegae, Y.
TITLE DNA comprising mutant FRT sequence
JOURNAL Patent: WO 0123545-A 3 05-APR-2001;
IZUMU SAITO, SUMITOMO PHARMACEUTICALS CO LTD, YUMI KANEGAE
COMMENT OS Saccharomyces cerevisiae (yeast)
PN WO 0123545-A/3
PD 05-APR-2001
PF 28-SEP-2000 WO 2000JP006686
PR 30-SEP-1999 JP 99P 280210, 06-DEC-1999 JP 99P 346727 PI

PC C12N15/11, C12N15/10, A01K67/027, A61K48/00
CC DNA comprising mutant FRT sequence
FH Key Location/Qualifiers
FT source 1..34
FT /organism='Saccharomyces cerevisiae (yeast)'.
FEATURES
source
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/mol_type='genomic DNA'
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ORIGIN
Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGTTCCTATCTCTCCAGAGAATAGGAATCTC 34
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GAAGTTCCTATCTCTCCAGAGAATAGGAATCTC 34

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 12:20:40 ; Search time 1692 Seconds
(without alignments)
764.885 Million cell updates/sec

Title: US-10-089-380-2

Perfect score: 34

Sequence: 1 gaagttctatactctctggagaatgaacttc 34

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	30.8	90.6	81	1	A1265023 uk01f07.y
C 3	30.8	90.6	81	1	A1265111 uk03c08.y
C 4	30.8	90.6	81	1	A1272501 uk04g01.y
C 5	30.8	90.6	88	1	A1316311 uj99a11.y
C 6	30.8	90.6	106	9	CG548652 OST150646
C 7	30.8	90.6	112	9	CG606396 OST284215
C 8	30.8	90.6	124	9	CG529627 OST110354
C 9	30.8	90.6	130	9	CG526837 OST103896
C 10	30.8	90.6	133	9	CG529602 OST102885
C 11	30.8	90.6	135	9	CG552967 OST164977
C 12	30.8	90.6	139	9	CG495088 OST34325
C 13	30.8	90.6	140	9	CG667250 OST459771
C 14	30.8	90.6	146	9	CG589974 OST242842
C 15	30.8	90.6	151	9	CG666807 OST457802
C 16	30.8	90.6	153	9	CG523992 OST97396
C 17	30.8	90.6	161	9	CG509937 OST291997
C 18	30.8	90.6	162	9	CG536645 OST124810
C 19	30.8	90.6	168	9	CG529685 OST110501
C 20	30.8	90.6	175	9	CR202574 Forward s
C 21	30.8	90.6	182	9	CG522772 OST92942
C 22	30.8	90.6	182	9	CG526410 OST102968
C 23	30.8	90.6	189	9	CG528753 OST108468
C 24	30.8	90.6	194	9	CG671483 OST500326

C 25	30.8	90.6	206	9	CG668768
C 26	30.8	90.6	208	9	CR069250
C 27	30.8	90.6	216	9	CG573772
C 28	30.8	90.6	216	9	CG579328
C 29	30.8	90.6	219	9	CG667178
C 30	30.8	90.6	222	9	CR271082
C 31	30.8	90.6	228	9	CG669744
C 32	30.8	90.6	239	9	CG667464
C 33	30.8	90.6	241	9	CG670326
C 34	30.8	90.6	253	9	CG527478
C 35	30.8	90.6	254	9	CG667921
C 36	30.8	90.6	279	9	CG670404
C 37	30.8	90.6	280	9	CG545746
C 38	30.8	90.6	281	9	CG667916
C 39	30.8	90.6	285	9	CG666517
C 40	30.8	90.6	285	9	CG666761
C 41	30.8	90.6	293	9	CG666889
C 42	30.8	90.6	306	9	CG666905
C 43	30.8	90.6	314	9	CG557567
C 44	30.8	90.6	314	9	CG668319
C 45	30.8	90.6	316	9	CG667495

ALIGNMENTS

RESULT 1
CG654127/c

LOCUS
OST420864

DEFINITION

CG654127

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 74

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129Sv/Ev"

/db_xref="taxon:10090"

/clone="OST420864"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129Sv/Ev"

Query Match

Best Local Similarity

Matches

32; Conservative

0; Mismatches

2; Indels

0; Gaps

0;

Qy

1 GAAGTTCCTACTCTCTGGAGAACTTC 34

Score 30.8; DB 9; Length 74;

Pred. No. 0.035;

0; Mismatches

2; Indels

0; Gaps

0;

Qy

1 GAAGTTCCTACTCTCTGGAGAACTTC 34

CG654127 74 bp mRNA linear GSS 02-OCT-2003
OST420864 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST420864,
mRNA sequence.

CG654127

CG654127.1 GI:37477976

GSS

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 74)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,

Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,

Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,

Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,

Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,

Sparks, M.J., Van Slightenhorst, I., Vogel, P., Walke, W., Xu, N.,

Zhu, Q., Person, C. and Sands, A.T.

Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap

screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as

described in Zambrowicz et al (Nature. 1998 Apr 9;393(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1. 74

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129Sv/Ev"

/db_xref="taxon:10090"

/clone="OST420864"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129Sv/Ev"

Query Match

Best Local Similarity

Matches

32; Conservative

0; Mismatches

2; Indels

0; Gaps

0;

Qy

1 GAAGTTCCTACTCTCTGGAGAACTTC 34

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 15:17:50 ; Search time 306.75 Seconds
(without alignments)
718.497 Million cell updates/sec

Title: US-10-089-380-2

Perfect score: 34

Sequence: 1 gaggtctctactctctggagaatggaacttc 34

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10J_NEW_PUB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
C 1	30.8	90.6	34	8	US-08-866-279A-14
C 2	30.8	90.6	34	9	US-09-920-932-2
C 3	30.8	90.6	34	9	US-09-804-653-7
C 4	30.8	90.6	34	9	US-09-748-739A-24
C 5	30.8	90.6	34	9	US-09-822-634-18
C 6	30.8	90.6	34	10	US-09-948-193-5
C 7	30.8	90.6	34	10	US-09-997-209-90

RESULT 1
US-08-866-279A-14/c
; Sequence 14, Application US/08866279A
; Publication No. US20020170076A1
; GENERAL INFORMATION:
; APPLICANT: Susan DYMECKI
; TITLE OF INVENTION: Use of Flp Recombinase in Mice
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866, 279A
; FILING DATE: 30-MAY-1997
; CLASSIFICATION: 800
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

ALIGNMENTS

C	8	30.8	90.6	34	13	US-10-086-542A-3	Sequence 3, Appli
C	9	30.8	90.6	34	15	US-10-005-602-5	Sequence 5, Appli
C	10	30.8	90.6	34	15	US-10-353-445-10	Sequence 10, Appl
C	11	30.8	90.6	34	16	US-10-368-442-7	Sequence 7, Appli
C	12	30.8	90.6	34	17	US-10-430-907-1	Sequence 1, Appli
C	13	30.8	90.6	34	17	US-10-430-908-1	Sequence 1, Appli
C	14	30.8	90.6	34	17	US-10-440-030-1	Sequence 1, Appli
C	15	30.8	90.6	34	17	US-10-378-064-4	Sequence 3, Appli
C	16	30.8	90.6	34	17	US-10-444-664-3	Sequence 1, Appli
C	17	30.8	90.6	34	18	US-10-639-751-1	Sequence 1, Appli
C	18	30.8	90.6	34	18	US-10-433-206-90	Sequence 90, Appl
C	19	30.8	90.6	34	19	US-10-649-547-19	Sequence 19, Appl
C	20	30.8	90.6	34	20	US-10-623-386-18	Sequence 18, Appl
C	21	30.8	90.6	34	20	US-10-846-700-14	Sequence 14, Appl
C	22	30.8	90.6	34	21	US-10-469-508-44	Sequence 44, Appl
C	23	30.8	90.6	34	21	US-10-976-042-39	Sequence 39, Appl
C	24	30.8	90.6	34	22	US-10-954-721-18	Sequence 18, Appl
C	25	30.8	90.6	42	10	US-09-843-150-24	Sequence 24, Appl
C	26	30.8	90.6	42	18	US-09-843-150-25	Sequence 25, Appl
C	27	30.8	90.6	42	18	US-10-270-176-55	Sequence 55, Appl
C	28	30.8	90.6	42	20	US-10-475-962-24	Sequence 24, Appl
C	29	30.8	90.6	42	20	US-10-475-962-25	Sequence 25, Appl
C	30	30.8	90.6	48	8	US-08-866-279A-15	Sequence 15, Appl
C	31	30.8	90.6	48	9	US-09-351-819-2	Sequence 2, Appli
C	32	30.8	90.6	48	15	US-10-206-163-2	Sequence 2, Appli
C	33	30.8	90.6	48	15	US-10-161-403-62	Sequence 62, Appl
C	34	30.8	90.6	48	15	US-10-161-403-63	Sequence 63, Appl
C	35	30.8	90.6	48	16	US-10-252-279-3	Sequence 3, Appli
C	36	30.8	90.6	48	20	US-10-846-700-15	Sequence 15, Appl
C	37	30.8	90.6	54	8	US-08-866-279A-3	Sequence 3, Appli
C	38	30.8	90.6	54	20	US-10-846-700-3	Sequence 3, Appli
C	39	30.8	90.6	58	10	US-09-843-150-32	Sequence 32, Appl
C	40	30.8	90.6	58	10	US-09-843-150-33	Sequence 33, Appl
C	41	30.8	90.6	58	16	US-10-182-616-29	Sequence 29, Appl
C	42	30.8	90.6	58	16	US-10-182-616-30	Sequence 30, Appl
C	43	30.8	90.6	58	20	US-10-475-962-32	Sequence 32, Appl
C	44	30.8	90.6	58	20	US-10-475-962-33	Sequence 33, Appl
C	45	30.8	90.6	59	8	US-08-866-279A-2	Sequence 2, Appli

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 13:28:42 ; Search time 59.5 Seconds
(without alignments)
935.015 Million cell updates/sec

Title: US-10-089-380-2

Perfect score: 34

Sequence: 1 gaggttctactctctggagaataggaacttc 34

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

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5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	30.8	90.6	34	1	US-08-484-324-3
C 2	30.8	90.6	34	1	US-08-486-409-3
C 3	30.8	90.6	34	2	US-08-864-224-18
C 4	30.8	90.6	34	2	US-08-975-763-3
C 5	30.8	90.6	34	2	US-08-825-784-3
C 6	30.8	90.6	34	2	US-08-972-258-4
C 7	30.8	90.6	34	3	US-09-011-257-2
C 8	30.8	90.6	34	3	US-08-745-404-5
C 9	30.8	90.6	34	3	US-09-263-128-4
C 10	30.8	90.6	34	3	US-09-193-502-1
C 11	30.8	90.6	34	3	US-09-193-503B-10
C 12	30.8	90.6	34	3	US-09-193-475-3
C 13	30.8	90.6	34	3	US-09-193-484-1
C 14	30.8	90.6	34	3	US-09-563-239-2
C 15	30.8	90.6	34	3	US-09-438-874A-1
C 16	30.8	90.6	34	3	US-09-439-158-1
C 17	30.8	90.6	34	4	US-09-415-839-10
C 18	30.8	90.6	34	4	US-09-718-034-1
C 19	30.8	90.6	34	4	US-09-606-323C-4
C 20	30.8	90.6	34	4	US-09-438-239-1
C 21	30.8	90.6	34	4	US-09-439-042A-1
C 22	30.8	90.6	34	4	US-09-455-050A-1
C 23	30.8	90.6	34	4	US-09-411-826-3
C 24	30.8	90.6	34	4	US-09-793-372-19
C 25	30.8	90.6	34	4	US-09-641-111A-4
C 26	30.8	90.6	34	4	US-09-869-185B-1
C 27	30.8	90.6	34	4	US-09-937-837-8

Sequence 14, Appl
Sequence 18, Appl
Sequence 3, Appl
Sequence 14, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 15, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-08-484-324-3/c
Sequence 3, Application US/08484324
Patent No. 5654182
GENERAL INFORMATION:
APPLICANT: Wahl, Geoffrey M.
TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL THEREFOR
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,324
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9984
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-324-3

Query Match 90.6%; Score 30.8; DB 1; Length 34;
Best Local Similarity 94.1%; Pred. No. 0.00024;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAGTTCCTACTCTCTGGAGAATAGGAACCTC 34
Db 34 GAAGTTCCTACTCTTCTAGAGAATAGGAACCTC 1

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 10:55:04 ; Search time 199 Seconds
(without alignments)
1011.413 Million cell updates/sec

Title: US-10-089-380-2
Perfect score: 34
Sequence: 1 gaagttctatctctctggagaataggaacttc 34

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*
1: geneseqn1990s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	34	4	Aaf87356 Yeast FRT
2	34	100.0	52	4	Aaf87372 Mutant FR
3	34	100.0	52	4	Aaf87381 Mutant FR
4	32.4	95.3	34	4	Aaf87359 Yeast FRT
5	32.4	95.3	52	4	Aaf87369 Mutant FR
6	32.4	95.3	52	4	Aaf87378 Mutant FR
7	30.8	90.6	34	2	Aaf92196 S. cerevi
8	30.8	90.6	34	2	Aav43562 FLP recom
9	30.8	90.6	34	2	Aax61227 Wild type
10	30.8	90.6	34	2	Aav72331 Wild type
11	30.8	90.6	34	2	Aax01426 2mu FRT e
12	30.8	90.6	34	2	Aai72854 Minimal F
13	30.8	90.6	34	3	Aaz58072 FLP recom
14	30.8	90.6	34	3	Aac61513 Nucleotid
15	30.8	90.6	34	3	Aaa10237 FLP recom
16	30.8	90.6	34	3	Aac63092 Mutant FR
17	30.8	90.6	34	3	Aac63090 Wild-type
18	30.8	90.6	34	3	Aaf24488 FLP recom
19	30.8	90.6	34	4	Aad10220 Minimal w
20	30.8	90.6	34	4	Aaf81218 FLP recom

21	30.8	90.6	34	4	Aaf87358	Yeast FRT
22	30.8	90.6	34	4	Aaf87357	Yeast FRT
23	30.8	90.6	34	4	Aaf87355	Yeast FRT
24	30.8	90.6	34	4	Aah21799	Saccharom
25	30.8	90.6	34	5	Aae14781	FLP recom
26	30.8	90.6	34	6	Aad46212	Yeast FRT
27	30.8	90.6	34	6	Aad24140	Recombina
28	30.8	90.6	34	6	AAD35275	FRT recog
29	30.8	90.6	34	6	ABA03777	Saccharom
30	30.8	90.6	34	6	AAD41158	Yeast tar
31	30.8	90.6	34	6	AAL49298	FLP recom
32	30.8	90.6	34	7	ADL18609	Frt site
33	30.8	90.6	34	8	ABX13963	Yeast FLP
34	30.8	90.6	34	8	ADAB8940	FLP recog
35	30.8	90.6	34	8	ABX93111	Minimal F
36	30.8	90.6	34	9	ACC85315	Recombina
37	30.8	90.6	34	9	ACD26382	FRT recom
38	30.8	90.6	34	10	ADC17306	Baker's Y
39	30.8	90.6	34	10	ADD13799	Oligonucl
40	30.8	90.6	34	10	ADD06116	Yeast fli
41	30.8	90.6	34	10	AAD61473	FLP recog
42	30.8	90.6	34	10	AD81223	FLP recom
43	30.8	90.6	34	10	ADFG5708	FLP-recog
44	30.8	90.6	34	10	ADG5098	FRT recom
45	30.8	90.6	34	10	ADH08623	Yeast FLP

ALIGNMENTS

RESULT 1
Aaf87356
ID Aaf87356 standard; DNA; 34 BP.
XX
AC Aaf87356;
XX
DT 09-JUL-2001 (first entry)
XX
DB Yeast FRT sequence variant #1.
XX
KW Yeast; FRT; gene therapy; gene insertion; gene replacement;
KW DNA recombination; recombinase; FLP; transgenic animal; variant; db.
OS Saccharomyces cerevisiae.
XX
FN WO200123545-A1.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-JP006686.
XX
PR 30-SEP-1999; 99JP-00280210.
PR 06-DEC-1999; 99JP-00346727.
(SUMU) SUMITOMO PHARM CO LTD.
(SAIT/) SAITO I.
PI Saito I, Kanegae Y;
XX
DR WPI, 2001-266149/27.
XX
PT Variant FRT sequences useful for in vivo gene therapy comprises central 8
base spacer sequence.
XX
XX
XX Disclosure; Page 57; 73pp; Japanese.
XX
CC The present sequence is a variant of the FRT sequence from Saccharomyces
cerevisiae. Variant FRT sequences may be used in a method of performing
highly efficient gene insertion or gene replacement. The variant FRT
sequences each undergo a recombination reaction with another variant FRT
of the same sequence in the presence of recombinase FLP. The method is
useful for producing transgenic animal cells and animals. By locally
inserting the DNA and recombinase FLP, genes can be targeted to specific

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 10:58:49 ; Search time 741.75 Seconds
(without alignments)
2221.068 Million cell updates/sec

Title: US-10-089-380-2

Perfect score: 34

Sequence: 1 gaggttctatactctctgagaataggaaatttc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	34	6	BD013285
2	34	100.0	52	6	BD013301
3	34	100.0	52	6	BD013310
4	32.4	95.3	34	6	BD013288
5	32.4	95.3	52	6	BD013298
6	32.4	95.3	52	6	BD013307
7	30.8	90.6	34	6	A59775
8	30.8	90.6	34	6	AR067801
9	30.8	90.6	34	6	ARI05498
10	30.8	90.6	34	6	ARI03039
11	30.8	90.6	34	6	ARI142481
12	30.8	90.6	34	6	BD246903
13	30.8	90.6	34	6	BD267670
14	30.8	90.6	34	6	C0813068
15	30.8	90.6	34	6	E43464
16	30.8	90.6	34	6	I59685
17	30.8	90.6	34	6	I69353
18	30.8	90.6	34	6	ARI194975
19	30.8	90.6	34	6	AR232395

C 20	30.8	90.6	34	6	AR234678	AR234678 Sequence
C 21	30.8	90.6	34	6	AR264370	AR264370 Sequence
C 22	30.8	90.6	34	6	AR302446	AR302446 Sequence
C 23	30.8	90.6	34	6	AR302544	AR302544 Sequence
C 24	30.8	90.6	34	6	AR307970	AR307970 Sequence
C 25	30.8	90.6	34	6	AR342117	AR342117 Sequence
C 26	30.8	90.6	34	6	AR370679	AR370679 Sequence
C 27	30.8	90.6	34	6	AR403690	AR403690 Sequence
C 28	30.8	90.6	34	6	AR438854	AR438854 Sequence
C 29	30.8	90.6	34	6	AR477307	AR477307 Sequence
C 30	30.8	90.6	34	6	AR494802	AR494802 Sequence
C 31	30.8	90.6	34	6	AR527595	AR527595 Sequence
C 32	30.8	90.6	34	6	AX101007	AX101007 Sequence
C 33	30.8	90.6	34	6	AX269147	AX269147 Sequence
C 34	30.8	90.6	34	6	AX359678	AX359678 Sequence
C 35	30.8	90.6	34	6	AX453121	AX453121 Sequence
C 36	30.8	90.6	34	6	AX55208	AX55208 Sequence
C 37	30.8	90.6	34	6	AX657059	AX657059 Sequence
C 38	30.8	90.6	34	6	AX657060	AX657060 Sequence
C 39	30.8	90.6	34	6	BD013284	BD013284 DNA compr
C 40	30.8	90.6	34	6	BD013286	BD013286 DNA compr
C 41	30.8	90.6	34	6	BD013287	BD013287 DNA compr
C 42	30.8	90.6	34	6	BD083074	BD083074 Antisense
C 43	30.8	90.6	34	6	BD093613	BD093613 Antisense
C 44	30.8	90.6	34	6	BD094631	BD094631 Method fo
C 45	30.8	90.6	35	6	BD271118	BD271118 Methods f

ALIGNMENTS

BD013285 34 bp DNA linear PAT 02-AUG-2002
DNA comprising mutant FRT sequence.

BD013285 1 GI:22093474

KEYWORDS WO 0123545-A/2.

Saccharomyces cerevisiae (baker's yeast)

Saccharomyces cerevisiae

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

REFERENCE 1 (bases 1 to 34)

AUTHORS Saito, I. and Kanegae, Y.

TITLE DNA comprising mutant FRT sequence

JOURNAL Patent: WO 0123545-A 2 05-APR-2001;

IZUMU SAITO, YUMI KANEGAE

OS Saccharomyces cerevisiae (yeast)

PN WO 0123545-A/2

PD 05-APR-2001

PF 28-SEP-2000 WO 2000JP006696

PR 30-SEP-1999 JP 99P 280210, 06-DEC-1999 JP 99P 346727 PI

PC C12N15/11, C12N15/10, A01K67/027, A61K48/00

CC DNA comprising mutant FRT sequence

EH Key Location/Qualifiers

FT source 1..34

FT Location/Qualifiers

FT /organism='Saccharomyces cerevisiae'

/mol_type='genomic DNA'

/db_xref='taxon:4932'

FEATURES

source

1..34

/organism='Saccharomyces cerevisiae'

/mol_type='genomic DNA'

/db_xref='taxon:4932'

ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 34;

Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGTTCTTACTCTCTCGAATAGGAATTC 34

Db 1 GAAGTTCTTACTCTCTCGAATAGGAATTC 34